AMENDMENTS TO THE SPECIFICATION

KMO 12-22-10

Please replace the paragraph on page 9, lines ~~8-11~~ 14-17, with the following paragraph:

Figure 3. The aligned amino acid sequence of the LjNFR5 and PsSYM10 proteins. ~~Amino acid residues sharing identity are highlighted.~~ The *Medicago truncatula* (Ac126779) showing 76 % amino acid ~~identy~~identity to *Lotus* NFR5 is included to exemplify a substantial identical protein sequence.

Please replace the third paragraph on page 17, lines 20-24:

Pfam consensus: a consensus sequence derived from a large collection of protein multiple sequence alignments and profile hidden Markov models used to identify conserved protein domains (Bateman *et al.,* 2002, Nucleic Acids Res. 30: 276-80; and searchable on the internet at ~~http://www.~~ sanger.ac.uk/Software/Pfam[[/]] and on NCBI at ~~http://www.~~ ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi.

with the following paragraph:

Pfam consensus: a consensus sequence derived from a large collection of protein multiple sequence alignments and profile hidden Markov models used to identify conserved protein domains (Bateman *et al.,* 2002, Nucleic Acids Res. 30: 276-80; and searchable on the internet at sanger.ac.uk/Software/Pfam and on NCBI at ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi.

KMO 12-22-10

Please replace the fourth paragraph on page 17, lines ~~26-30~~ 25-30:

Protein domain prediction: sequences are analyzed by BLAST (~~www.~~ (ncbi.nlm.nih.gov/BLAST[[/]]) and PredictProtein (~~www.~~ (emblheidelberg.de/predictprotein/predictprotein). Signal peptides are predicted by

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Substantially identical: refers to two nucleic acid or polypeptide sequences that have at least about 60%, preferably about 65%, more preferably about 70%, further more preferably about 80%, most preferably about 90 or about 95% nucleotide or amino acid residue identity when aligned for maximum correspondence over a comparison window as measured using one of the sequence comparison algorithms given herein, or by manual alignment and visual inspection. This definition also refers to the complement of the test sequence with respect to its substantial identity to a reference sequence. A comparison window refers to any one of the number of contiguous positions in a sequence (being anything from between about 20 to about 600, most commonly about 100 to about 150) which may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment can be achieved using computerized implementations of alignment algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. USA) or BLAST analyses available on the site: ncbi.nlm.nih.gov.

KMD
12-22-10

Please replace the paragraph on page 53, lines ~~17-22~~ 26-29 through pg. 54 lines. 1-2, with the following:

Molecular markers based on DNA polymorphism are used to detect the alleles in breeding populations. Similar use can be taken of the *NFR1* sequences. Molecular DNA markers, based on the *NFR5* allele sequence differences of *Lotus* and pea, are bolded in Table 12 and highlighted in ~~Tables 12 and~~Table 13 as examples of how DNA polymorphism can be used directly to detect the presence of an advantageous allele in a breeding population.

Please replace Table 1 on page 55 with the following:

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AMENDMENTS TO THE SPECIFICATION

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Please replace the paragraph starting on page 8, line ~~21~~ 27 – page 9, line ~~7~~ 13, with the following:

Figure 2: Structure and domains of the NFR5 protein. **a.** Schematic representation of the NFR5 protein domains. **b.** The amino acid sequence of NFR5 arranged in protein domains. Bold, conserved LysM residues. Bold and underlined residues conserved in protein kinase domains (KD); TM: transmembrane, SP: signal peptide. The asterisk indicates a stop codon in the *nfr5-3*; the black triangle a retrotransposon insertion in *nfr5-2* and the ~~grey~~ box defines the amino acids deleted in *nfr5-1*. **c.** Individual alignment of the three LysM motifs (M1, M2, M3) from NFR5, pea SYM10, *Medicago truncatula* (*M.t*, Ac126779) rice (Ac103891), the single LysM in chitinase from *Volvox carteri* (Acc. No: T08150) and the pfam consensus. **d.** The divergent or absent activation loop (domain VIII) in the NFR5 family of receptor kinases is illustrated by alignment of kinase motifs VII, VIII and IX from *Arabidopsis* (At2g33580) NFR5, SYM10, *Medicago truncatula* (*M.t*, Ac126779), rice (Ac103891) and the SMART consensus. Conserved domain VII aspartic acid is marked in bold and underlined. In Figures **2c** and **d**, the amino acids conserved in all aligned motifs are marked in ~~black~~ bold and amino acids conserved in two or more motifs are ~~marked in grey~~ underlined.

KMO 12-22-10

Please replace the paragraph starting on page 9, line ~~22~~ 29 – page 10, line ~~8~~ 14, with the following:

Figure 5. Positional cloning of the *NFR1* gene. ~~a.~~ Genetic map of the region surrounding the *NFR1* locus. Positions of the closest AFLP, microsatellite- and PCR-markers are given together with genetic distances in cM. **b.** Physical map of the *NFR1* locus. BAC clones 56L2, 16K18, 10M24, 36D15, 56K22 and TAC clones LjT05B16, LjT02D13, LjT211O02, which cover the region are shown. The numbers of recombination events detected with BAC and TAC end-markers or internal markers are given. Arrows indicate the positions of the